

SEQUENCE LISTING

<110> Nakamura, Yusuke
Katagiri, Toyomasa

<120> GENES AND POLYPEPTIDES RELATING TO HUMAN
MYELOID LEUKEMIA

<130> 082368-003910US

<140> 10/530,217

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<150> PCT/JP03/09589

<151> 2003-07-29

<150> US 60/414,867

<151> 2002-09-30

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 sequence for antisense

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Met Ser
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gag gcc cgc agg gac agc acg agc agc ctg cag cgc aag aag cca ccc 164
Glu Ala Arg Arg Asp Ser Thr Ser Ser Leu Gln Arg Lys Lys Pro Pro
5 10 15

tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag 212
Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
20 25 30

ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg 260
Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
35 40 45 50

agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 308
Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
55 60 65_

cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc 356
Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
70 75 80

agg ggg acc gcc gac tgg ttt gga gtg agc aag gac agt gac agc acc 404
Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp Ser Thr
85 90 95

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Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg Tyr Gly
100 105 110

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Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
115 120 125 130

aac gtg tcg ctg acc agc acc gag acg cca ccc cca ctc tac gtg ggg 548
Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr Val Gly
135 140 145

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Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly

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cgt gcc ttc	cgt gtg gca gat	gac act gcg gaa ggc	ctg agt gcc cca	644								
Arg Ala Phe	Arg Val Ala Asp	Asp Thr Ala Glu Gly	Leu Ser Ala Pro									
165		170	175									
cac act ccc	gtc acg ccg ggt	gct gcc tcc ctc	tgc tcc ttc tcc agc	692								
His Thr Pro	Val Thr Pro Gly	Ala Ala Ser Leu	Cys Ser Phe Ser Ser									
180	185		190									
tcc cgc tca	ggt ttc cac cgg	ctc ccg cgg cgg	cgc aag cga gag tcg	740								
Ser Arg Ser	Gly Phe His Arg	Leu Pro Arg Arg	Lys Arg Glu Ser									
195	200	205	210									
gtg gcc aag	atg agc ttc cgg	gcg gcc gca gcg	ctg atg aaa ggc cgc	788								
Val Ala Lys	Met Ser Phe Arg	Ala Ala Ala Ala	Leu Met Lys Gly Arg									
	215	220	225									
tcc gtt agg	gat ggc acc ttt	cgc cgg gca cgg	cgt cga agc ttc act	836								
Ser Val Arg	Asp Gly Thr Phe	Arg Arg Ala Arg	Arg Arg Ser Phe Thr									
	230	235	240									
cca gct agc	ttt ctg gag gag	gac aca act gat	ttc ccc gat gag ctg	884								
Pro Ala Ser	Phe Leu Glu Glu	Asp Thr Thr Asp	Phe Pro Asp Glu Leu									
	245	250	255									
gac aca tcc	ttc ttt gcc cgg	gaa ggt atc ctc	cat gaa gag ctg tcc	932								
Asp Thr Ser	Phe Phe Ala Arg	Glu Gly Ile Leu	His Glu Glu Leu Ser									
260	265	270										
aca tac ccg	gat gaa gtt ttc	gag tcc cca tcc	gag gca gcg cta aag	980								
Thr Tyr Pro	Asp Glu Val Phe	Glu Ser Pro Ser	Glu Ala Ala Leu Lys									
275	280	285	290									
gac tgg gag	aag gca ccg gag	cag gcg gac ctc	acc ggc ggg gcc ctg	1028								
Asp Trp Glu	Lys Ala Pro Glu	Gln Ala Asp Leu	Thr Gly Gly Ala Leu									
	295	300	305									
gac cgc agc	gag ctt gag cgc	agc cac ctg atg	ctg ccc ttg gag cga	1076								
Asp Arg Ser	Glu Leu Glu Arg	Ser His Leu Met	Leu Pro Leu Glu Arg									
	310	315	320									
ggc tgg cgg	aag cag aag gag	ggc gcc gca gcc	ccg cag ccc aag gtg	1124								
Gly Trp Arg	Lys Gln Lys Glu	Gly Ala Ala Ala	Pro Gln Pro Lys Val									
325	330	335										
cgg ctc cga	cag gag gtg gtg	agc acc gcg ggg	ccg cga cgg ggc cag	1172								
Arg Leu Arg	Gln Glu Val Val	Ser Thr Ala Gly	Pro Arg Arg Gly Gln									
340	345	350										
cgt atc gcg	gtg ccg gtg cgc	aag ctc ttc gcc	cgg gag aag cgg ccg	1220								
Arg Ile Ala	Val Pro Val Arg	Lys Leu Phe Ala	Arg Glu Lys Arg Pro									
355	360	365	370									
tat ggg ctg	ggc atg gtg gga	cgg ctc acc aac	cgc acc tac cgc aag	1268								
Tyr Gly Leu	Gly Met Val Gly	Arg Leu Thr Asn	Arg Thr Tyr Arg Lys									
	375	380	385									
cgc atc gac	agc ttc gtc aag	cgc cag atc gag	gac atg gac gac cac	1316								
Arg Ile Asp	Ser Phe Val Lys	Arg Gln Ile Glu	Asp Met Asp Asp His									
	390	395	400									

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Arg Pro Phe Phe Thr Tyr Trp Leu Thr Phe Val His Ser Leu Val Thr	
405 410 415	
atc cta gcc gtg tgc atc tat ggc atc gcg ccc gtg ggc ttc tcg cag	1412
Ile Leu Ala Val Cys Ile Tyr Gly Ile Ala Pro Val Gly Phe Ser Gln	
420 425 430	
cat gag acg gtg gac tcg gtg ctg cgg aac cgc ggg gtc tac gag aac	1460
His Glu Thr Val Asp Ser Val Leu Arg Asn Arg Gly Val Tyr Glu Asn	
435 440 445 450	
gtc aag tac gtg cag cag gag aac ttc tgg atc ggg ccc agc tcg gag	1508
Val Lys Tyr Val Gln Gln Glu Asn Phe Trp Ile Gly Pro Ser Ser Glu	
455 460 465	
gcc ctc atc cac ctg ggc gcc aag ttt tcg ccc tgc atg cgc cag gac	1556
Ala Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys Met Arg Gln Asp	
470 475 480	
ccg cag gtg cac agc ttc att cgc tcg gcg cgc gag cgc gag aag cac	1604
Pro Gln Val His Ser Phe Ile Arg Ser Ala Arg Glu Arg Glu Lys His	
485 490 495	
tcc gcc tgc tgc gtg cgc aac gac agg tcg ggc tgc gtg cag acc tcg	1652
Ser Ala Cys Cys Val Arg Asn Asp Arg Ser Gly Cys Val Gln Thr Ser	
500 505 510	
gag gag gag tgc tcg tcc acg ctg gca gtg tgg gtg aag tgg ccc atc	1700
Glu Glu Glu Cys Ser Ser Thr Leu Ala Val Trp Val Lys Trp Pro Ile	
515 520 525 530	
cat ccc agc gcc cca gag ctt gcg ggc cac aag aga cag ttt ggc tct	1748
His Pro Ser Ala Pro Glu Leu Ala Gly His Lys Arg Gln Phe Gly Ser	
535 540 545	
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Val Cys His Gln Asp Pro Arg Val Cys Asp Glu Pro Ser Ser Glu Asp	
550 555 560	
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Pro His Glu Trp Pro Glu Asp Ile Thr Lys Trp Pro Ile Cys Thr Lys	
565 570 575	
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Asn Ser Ala Gly Asn His Thr Asn His Pro His Met Asp Cys Val Ile	
580 585 590	
aca gga cgg ccc tgc tgc att ggc acc aag ggc agg tgt gag atc acc	1940
Thr Gly Arg Pro Cys Cys Ile Gly Thr Lys Gly Arg Cys Glu Ile Thr	
595 600 605 610	
tcc cgg gag tac tgt gac ttc atg agg ggc tac ttc cat gag gag gcc	1988
Ser Arg Glu Tyr Cys Asp Phe Met Arg Gly Tyr Phe His Glu Glu Ala	
615 620 625	
acg ctc tgc tct cag gtg cac tgc atg gat gat gtg tgt ggg ctc ctg	2036
Thr Leu Cys Ser Gln Val His Cys Met Asp Asp Val Cys Gly Leu Leu	
630 635 640	

cct ttt ctc aac ccc gag gtg cct gac cag ttc tac cgc ctg tgg cta	2084
Pro Phe Leu Asn Pro Glu Val Pro Asp Gln Phe Tyr Arg Leu Trp Leu	
645 650 655	
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Ser Leu Phe Leu His Ala Gly Ile Leu His Cys Leu Val Ser Ile Cys	
660 665 670	
ttc cag atg act gtc ctg cgg gac ctg gag aag ctg gca gcc tgg cac	2180
Phe Gln Met Thr Val Leu Arg Asp Leu Glu Lys Leu Ala Gly Trp His	
675 680 685 690	
cgc ata gcc atc atc tac ctg ctg agt ggt gtc acc gcc aac ctg gcc	2228
Arg Ile Ala Ile Ile Tyr Leu Leu Ser Gly Val Thr Gly Asn Leu Ala	
695 700 705	
agt gcc atc ttc ctg cca tac cga gca gag gtg ggt cct gct gcc tcc	2276
Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu Val Gly Pro Ala Gly Ser	
710 715 720	
cag ttc gcc atc ctg gcc tgc ctc ttc gtg gag ctc ttc cag agc tgg	2324
Gln Phe Gly Ile Leu Ala Cys Leu Phe Val Glu Leu Phe Gln Ser Trp	
725 730 735	
cag atc ctg gcg cgg ccc tgg cgt gcc ttc ttc aag ctg ctg gct gtg	2372
Gln Ile Leu Ala Arg Pro Trp Arg Ala Phe Phe Lys Leu Leu Ala Val	
740 745 750	
gtg ctc ttc ctc ttc acc ttt ggg ctg ctg ccg tgg att gac aac ttt	2420
Val Leu Phe Leu Phe Thr Phe Gly Leu Leu Pro Trp Ile Asp Asn Phe	
755 760 765 770	
gcc cac atc tcg ggg ttc atc agt ggc ctc ttc ctc tcc ttc gcc ttc	2468
Ala His Ile Ser Gly Phe Ile Ser Gly Leu Phe Leu Ser Phe Ala Phe	
775 780 785	
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Leu Pro Tyr Ile Ser Phe Gly Lys Phe Asp Leu Tyr Arg Lys Arg Cys	
790 795 800	
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Gln Ile Ile Ile Phe Gln Val Val Phe Leu Gly Leu Leu Ala Gly Leu	
805 810 815	
gtg gtc ctc ttc tac gtc tat cct gtc cgc tgt gag tgg tgt gag ttc	2612
Val Val Leu Phe Tyr Val Tyr Pro Val Arg Cys Glu Trp Cys Glu Phe	
820 825 830	
ctc acc tgc atc ccc ttc act gac aag ttc tgt gag aag tac gaa ctg	2660
Leu Thr Cys Ile Pro Phe Thr Asp Lys Phe Cys Glu Lys Tyr Glu Leu	
835 840 845 850	
gac gct cag ctc cac tga gctggctgcg ggctccagcg gccgtgtgct	2708
Asp Ala Gln Leu His *	
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cattaacttg 2958

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35 40 45
Ser Val Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His
50 55 60
Glu Leu Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr
65 70 75 80
Ile Arg Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp
85 90 95
Ser Thr Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg
100 105 110
Tyr Gly Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser
115 120 125
Gln Asp Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr
130 135 140
Val Gly Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala
145 150 155 160
Arg Gly Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser
165 170 175
Ala Pro His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe
180 185 190
Ser Ser Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg
195 200 205
Glu Ser Val Ala Lys Met Ser Phe Arg Ala Ala Ala Leu Met Lys
210 215 220
Gly Arg Ser Val Arg Asp Gly Thr Phe Arg Arg Ala Arg Arg Arg Ser
225 230 235 240
Phe Thr Pro Ala Ser Phe Leu Glu Glu Asp Thr Thr Asp Phe Pro Asp
245 250 255
Glu Leu Asp Thr Ser Phe Phe Ala Arg Glu Gly Ile Leu His Glu Glu
260 265 270
Leu Ser Thr Tyr Pro Asp Glu Val Phe Glu Ser Pro Ser Glu Ala Ala
275 280 285
Leu Lys Asp Trp Glu Lys Ala Pro Glu Gln Ala Asp Leu Thr Gly Gly
290 295 300
Ala Leu Asp Arg Ser Glu Leu Glu Arg Ser His Leu Met Leu Pro Leu
305 310 315 320
Glu Arg Gly Trp Arg Lys Gln Lys Glu Gly Ala Ala Ala Pro Gln Pro
325 330 335
Lys Val Arg Leu Arg Gln Glu Val Val Ser Thr Ala Gly Pro Arg Arg
340 345 350
Gly Gln Arg Ile Ala Val Pro Val Arg Lys Leu Phe Ala Arg Glu Lys
355 360 365
Arg Pro Tyr Gly Leu Gly Met Val Gly Arg Leu Thr Asn Arg Thr Tyr
370 375 380
Arg Lys Arg Ile Asp Ser Phe Val Lys Arg Gln Ile Glu Asp Met Asp
385 390 395 400
Asp His Arg Pro Phe Phe Thr Tyr Trp Leu Thr Phe Val His Ser Leu

